

Serial Number: 09/733,685

CRF Processing Date: 12/21/2000

Edited by:

Verified by:

(STIC Staff)

Changed a file from non-ASCII to ASCII

Changed the margins in cases where the sequence text was wrapped down to the next line.

Edited a format error in the Current Application Data section, specifically:

ENTERED

H2
0430
3/27/01

Edited the Current Application Data section with the actual current number. The number inputted by the applicant was the prior application data; or other _____.

Added the mandatory heading and subheadings for "Current Application Data".

Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

Changed the spelling of a mandatory field (the headings or subheadings), specifically:

Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

Inserted colons after headings/subheadings. Headings edited included:

Deleted extra, invalid, headings used by an applicant, specifically:

Deleted: non-ASCII "garbage" at the beginning/end of files; secretary initials/filename at end of file; page numbers throughout text; other invalid text, such as _____.

Inserted mandatory headings, specifically: _____

Corrected an obvious error in the response, specifically:

Edited identifiers where upper case is used but lower case is required, or vice versa.

Corrected an error in the Number of Sequences field, specifically:

A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

Other: Segr 22-23 - inserted hard returns

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/733,685
 DATE: 12/21/2000
 TIME: 10:14:24
 Input Set : A:\seq-list.txt
 Output Set: N:\CRF3\12212000\I733685.raw

Does Not Comp'y
 Corrected Diskette Needed

3 <110> APPLICANT: Cade, Rebecca M
 4 Dietrich, Robert A
 6 <120> TITLE OF INVENTION: GENES ENCODING PROTEINS INVOLVED IN THE REGULATION OF
 7 SAR GENE EXPRESSION IN PLANTS
 9 <130> FILE REFERENCE: A-31089A
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/733,685
 C--> 12 <141> CURRENT FILING DATE: 2000-12-08
 14 <150> PRIOR APPLICATION NUMBER: 60/171,008
 15 <151> PRIOR FILING DATE: 1999-12-15
 17 <150> PRIOR APPLICATION NUMBER: 60/175,519
 18 <151> PRIOR FILING DATE: 2000-01-11
 20 <160> NUMBER OF SEQ ID NOS: 23
 22 <170> SOFTWARE: PatentIn Ver. 2.1
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 509
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Arabidopsis thaliana
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (68)..(433)
 32 <223> OTHER INFORMATION: gene product NIL6
 34 <220> FEATURE:
 35 <221> NAME/KEY: misc_feature
 36 <222> LOCATION: (142)..(147)
 37 <223> OTHER INFORMATION: Sali site
 39 <220> FEATURE:
 40 <221> NAME/KEY: misc_feature
 41 <222> LOCATION: (344)..(349)
 42 <223> OTHER INFORMATION: EcoRI site
 44 <400> SEQUENCE: 1
 45 aaaatcaga aataaactt tcttgactaa gcttaaacga cggccgttaac attttcttct 60
 47 ggcttaac atq aac aac tct ttg aag aaa gaa gaa cgc gta gaa gaa gat 109
 48 Met Asn Asn Ser Ileu Lys Lys Glu Glu Arg Val Glu Glu Asp
 49 1 5 10
 51 aac gga aaa tct gac ggt aac aga ggg aaa ccg tct acg gaa gtt gtt 157
 52 Asn Gly Lys Ser Asp Gly Asn Arg Gly Lys Pro Ser Thr Glu Val Val
 53 15 20 25 30
 55 cgg acg gta acg gag gaa gag gtg gat gag ttt ttc aag ata tta cgg 205
 56 Arg Thr Val Thr Glu Glu Val Asp Glu Phe Phe Lys Ile Leu Arg
 57 35 40 45
 59 aga gta cac gtg gct aca cga acg gtt gct aaa gtt aac ggc ggt gtt 253
 60 Arg Val His Val Ala Thr Arg Thr Val Ala Lys Val Asn Gly Val
 61 50 55 60
 63 gct gag gga gag tta ccg tct aag aag agg aaa ccg aat ctt 301
 64 Ala Glu Gly Glu Leu Pro Ser Lys Lys Arg Lys Arg Ser Gln Asn Leu
 65 65 70 75
 67 ggg ttg aga aac tct ttg gat tgt aac ggc gtt cga gac gga gaa ttc 349

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68 Gly Leu Arg Asn Ser Leu Asp Cys Asn Gly Val Arg Asp Gly Glu Phe
69 80 85 90
71 qat qaq att aat cqq qtc ggg tta caq qqt ttq gqt ttq qat ctq aac 397
72 Asp Glu Ile Asn Arg Val Gly Leu Gln Gly Leu Gly Leu Asp Leu Asn
73 95 100 105 110
75 tgt aaa ccg gaa cca gac agc gtt aqt tta tcg ttg tagacttgta 413
76 Cys Lys Pro Glu Pro Asp Ser Val Ser Leu Ser Leu
77 115 120
79 gtccttcatg tttttccct tcttacuata atcaattttt tttaactac aatactttt 503
81 aaaaaa 509
84 <210> SEQ ID NO: 2
85 <211> LENGTH: 122
86 <212> TYPE: PRT
87 <213> ORGANISM: Arabidopsis thaliana
89 <400> SEQUENCE: 2
90 Met Asn Asn Ser Leu Lys Lys Glu Glu Arg Val Glu Glu Asp Asn Gly
91 1 5 10 15
93 Lys Ser Asp Gly Asn Arg Gly Lys Pro Ser Thr Glu Val Val Arg Thr
94 20 25 30
96 Val Thr Glu Glu Glu Val Asp Glu Phe Phe Lys Ile Leu Arg Arg Val
97 35 40 45
99 His Val Ala Thr Arg Thr Val Ala Lys Val Asn Gly Gly Val Ala Glu
100 50 55 60
102 Gly Glu Leu Pro Ser Lys Lys Arg Lys Arg Ser Gln Asn Leu Gly Leu
103 65 70 75 80
105 Arg Asn Ser Leu Asp Cys Asn Gly Val Arg Asp Gly Glu Phe Asp Glu
106 85 90 95
108 Ile Asn Arg Val Gly Leu Gln Gly Leu Gly Leu Asp Leu Asn Cys Lys
109 100 105 110
111 Pro Glu Pro Asp Ser Val Ser Leu Ser Leu
112 115 120
116 <210> SEQ ID NO: 3
117 <211> LENGTH: 1700
118 <212> TYPE: DNA
119 <213> ORGANISM: Arabidopsis thaliana
121 <220> FEATURE:
122 <221> NAME/KEY: misc_feature
123 <222> LOCATION: (365)..(374)
124 <223> OTHER INFORMATION: TCAL motif
126 <220> FEATURE:
127 <221> NAME/KEY: misc_feature
128 <222> LOCATION: (426)..(435)
129 <223> OTHER INFORMATION: TCAL motif
131 <220> FEATURE:
132 <221> NAME/KEY: misc_feature
133 <222> LOCATION: (609)..(614)
134 <223> OTHER INFORMATION: MYCATR22 element
136 <220> FEATURE:
137 <221> NAME/KEY: misc_feature

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194 <221> NAME/KEY: CDS
195 <222> LOCATION: (124)..(438)
197 <400> SEQUENCE: 4
198 caaaggataac acacagaaaa cattgacata acaqatcgaa tacacattat attatattaa 60
200 tgagagaata aagagaagta attgcctctag cagtattgc aattaatcg ctgcggct 120
202 tga atg cta ctt atq gac gga gaa aag aag agg aag aca gca atc 168
203 Met Leu Ile Met Asp Gly Lys Lys Arg Lys Arg Thr Ala Ile
204 1 5 10 15
206 ggc gcc qqa qat cqg agt aag qat qaa gta gaa gct act gtg aag gag 216
207 Gly Ala Gly Asp Arg Ser Lys Asp Glu Val Ala Thr Val Lys Glu
208 20 25 30
210 qaa gag ccq ccq tca qaa qcc qaa gtt qac gag ttc ttc qcg atc tta 264
211 Glu Glu Pro Pro Ser Glu Ala Glu Val Asp Glu Phe Phe Ala Ile Leu
212 35 40 45
214 cgg agg alq cat qtq qcq qtq aad tat ctc caq aqa aat gct cag att 312
215 Arg Arg Met His Val Ala Val Lys Tyr Leu Gln Arg Asn Ala Glu Ile
216 50 55 60
218 cgg qaa aac ctt aac qca tcq ccq gcc qgt gct aac qgt gtc qca 360
219 Arg Pro Glu Asn Leu Asn Ala Ser Pro Ala Gly Ala Asn Gly Val Ala
220 65 70 75
222 qct qja cgg aag aqa gaa cgg qga atc qtq aqa aaa ggt gat ttq gac 408
223 Ala Gly Arg Lys Arg Glu Arg Gly Ile Val Arg Lys Gly Asp Leu Asp
224 80 85 90 95
226 ctc aac act ctg ccq qac qcc qga gac taa tttaacgcagt tttaaggcatag 458
227 leu Asn Thr Leu Pro Asp Gly Gly Asp
W--> 228 100 105
230 gtttaattaca taaatgcacc ctttaattatc attagattttt aqattgtatc tqctgtacag 518
232 atttaattat taaaggccctt tttttatatac ttatctccgg taaacggttt gcttttg 578
234 attttcttta ataaatttaa ttattttat 608
237 <210> SEQ ID NO: 5
238 <211> LENGTH: 104
239 <212> TYPE: PRT
240 <213> ORGANISM: Solanum tuberosum
242 <400> SEQUENCE: 5
243 Met Leu Leu Met Asp Gly Glu Lys Lys Arg Lys Arg Thr Ala Ile Gly
244 1 5 10 15
245 Ala Gly Asp Arg Ser Lys Asp Glu Val Ala Thr Val Lys Glu Glu
246 20 25 30
247 Glu Pro Pro Ser Glu Ala Glu Val Asp Glu Phe Phe Ala Ile Leu Arg
248 35 40 45
249 Arg Met His Val Ala Val Lys Tyr Leu Gln Arg Asn Ala Gln Ile Arg
250 50 55 60
251 Pro Glu Asn Leu Asn Ala Ser Pro Ala Gly Ala Asn Gly Val Ala Ala
252 65 70 75 80
253 Gly Arg Lys Arg Glu Arg Gly Ile Val Arg Lys Gly Asp Leu Asp Leu
254 85 90 95
255 Asn Thr Leu Pro Asp Gly Gly Asp
256 100
260 <210> SEQ ID NO: 6

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Input Set : A:\seq-list.txt
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261 <211> LENGTH: 349
262 <212> TYPE: DNA
263 <213> ORGANISM: Lycopersicon esculentum
265 <220> FEATURE:
266 <221> NAME/KEY: CDS
267 <222> LOCATION: (3)..(233)
269 <400> SEQUENCE: 6
270 ct tcg qag qga gag qtg gat qag ttt ttc gca att tta cgg agg atg 47
271 Ser Glu Gly Glu Val Asp Glu Phe Phe Ala Ile Leu Arg Arg Met
272 1 5 10 15
274 cac atg gcc gta aaa tat ctt cag aca aac qct cag att cag ccc qaa 95
275 His Met Ala Val Lys Tyr Leu Gln Arg Asn Ala Gln Ile Gln Pro Glu
276 20 25 30
278 aac qtt aac gct cac ggc aac aag tta acc gca tcg cgg gcc qgt qtt 143
279 Asn Val Asn Ala His Gly Ser Lys Leu Thr Ala Ser Pro Ala Gly Val
280 35 40 45
282 aac gga qat gca act gga cag aac qaa cgg cgg qga atc qtg aga aaa 191
283 Asn Gly Asp Ala Thr Gly Gin Lys Arg Glu Arg Gly Ile Val Arg Lys
284 50 55 60
286 qgt qat ttc gac ctc aac act ttc cgg qac ttc gca qac taa 233
287 Gly Asp Leu Asp Leu Asn Thr Ile Pro Asp Cys Gly Asp
288 65 70 75
290 cgcacgtttaa gcataggtaa attacagaaa tgcaccccttaa attatcgtag attcttaaga 293
292 ttcgttgcgtt qtaaaaaatgaa attaaatgaa gcctttttt atatataaaa aaaaaaa 349
295 <210> SEQ ID NO: 7
296 <211> LENGTH: 76
297 <212> TYPE: PRT
298 <213> ORGANISM: Lycopersicon esculentum
300 <400> SEQUENCE: 7
301 Ser Glu Gly Glu Val Asp Glu Phe Phe Ala Ile Leu Arg Arg Met His
302 1 5 10 15
303 Met Ala Val Lys Tyr Leu Gln Arg Asn Ala Gln Ile Gln Pro Glu Asn
304 20 25 30
305 Val Asn Ala His Gly Ser Lys Leu Thr Ala Ser Pro Ala Gly Val Asn
306 35 40 45
307 Gly Asp Ala Thr Gly Gln Lys Arg Glu Arg Gly Ile Val Arg Lys Gly
308 50 55 60
309 Asp Leu Asp Leu Asn Thr Ile Pro Asp Cys Gly Asp
310 65 70 75
314 <210> SEQ ID NO: 8
315 <211> LENGTH: 75
316 <212> TYPE: PRT
317 <213> ORGANISM: Glycine max
319 <400> SEQUENCE: 8
320 Met Glu Val Glu Lys Arg Lys Asn Lys Arg Val Met Gly Glu Glu
321 1 5 10 15
323 Glu Ser Glu Arg Val Lys Asn Lys Arg Leu Lys Gly Val Glu Glu Glu
324 20 25 30
326 Asp Gly Ser Asp Gly Val Pro Thr Glu Glu Val Glu Glu Phe Phe

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/733,685 DATE: 12/21/2000
TIME: 10:14:25

Input Set : A:\seq-list.txt
Output Set: N:\CRF3\12212000\I733685.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:228 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:512 M:341 W: (46) "n" or "Xaa" used, for SEQ ID:20
L:530 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:534 M:283 W: Missing Blank Line separator, <220> field identifier
L:534 M:282 W: Invalid Numeric Header Field, <220> has non-blank data
L:535 M:282 W: Numeric Field Identifier Missing, <211> is required.
L:535 M:282 W: Numeric Field Identifier Missing, <212> is required.
L:535 M:282 W: Numeric Field Identifier Missing, <213> is required.
L:535 M:283 W: Missing Blank Line separator, <400> field identifier
L:570 M:282 W: Numeric Field Identifier Missing, <211> is required.
L:570 M:282 W: Numeric Field Identifier Missing, <212> is required.
L:570 M:282 W: Numeric Field Identifier Missing, <213> is required.
L:570 M:283 W: Missing Blank Line separator, <400> field identifier